

09500746-030900

FIG. 1

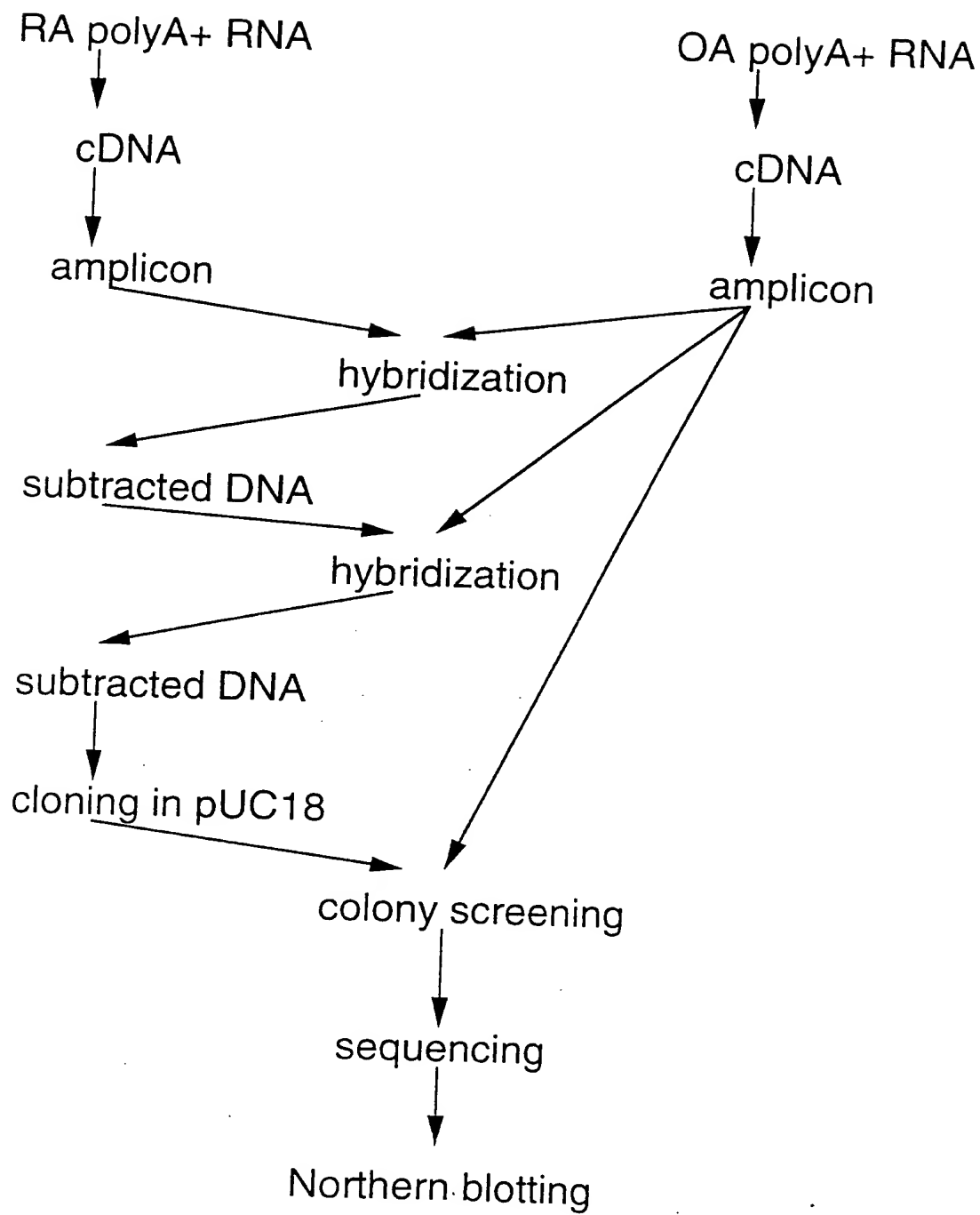
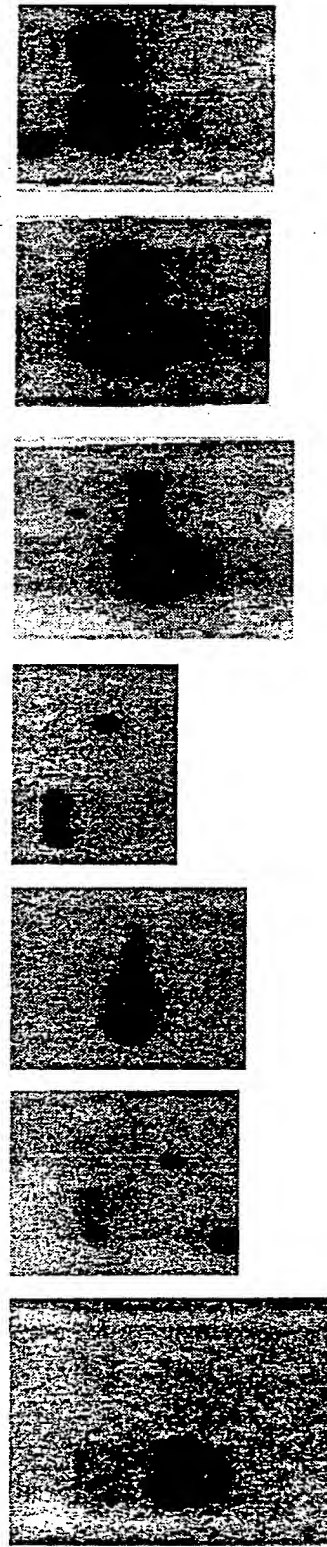


FIG. 2

SAVCVYHLS	DIQ	TVFNGPFAHKEGPNHQ	LISYQGR	I	PYP	R	m	semaphor	in E	
SAVCVYHLS	DIQ	TVFNGPFAHKEGPNHQ	LISYQGR	I	PYP	R	h	semaphor	in VI	
SAVCVYSMA	DIR	TVFNGPFAHKEGPNHQ	WMPFS	GKM	PYP	R	h	semaphor	in IV	
SAVCVYSMN	DVRR	AFELGPF	FAHKEGPNHQ	WVS	YQGR	VYPR	h	semaphor	in V	
SAVCMYSMS	DVRR	VEFGP	YAHKEGPNHQ	WVS	YQGR	VYPR	h	semaphor	in II	
PGTCPGG	AETPNM	RTTKDFFPDDV	VVTF	IRNHPLMYNS	I	SP	I	m	semaphor	in E
PGTCPGG	ALTPNM	RTTKDFFPDDV	VVTF	IRNHPLMYNS	I	YP	I	h	semaphor	in VI
PGTCPGG	TFTPSM	KSTKDYPPDE	VIN	FM	RRSHPLMYQAV	V	P	h	semaphor	in IV
PGMCP	SKTFTGTF	SGTFSX	STKDEFPDDV	ILQF	ARNHPLMYNS	V	L	h	semaphor	in V
PGTCP	SKTEGGFD	STKDL	LPDDV	ITFA	SHPLMYNP	V	F	h	semaphor	in II
HRRL	I	VRIG	TDYK	YTK	YTK	YTK	YTK	m	semaphor	in E
HRRL	I	VRIG	TDYK	YTK	YTK	YTK	YTK	h	semaphor	in VI
QRRL	VVR	TGAP	YR	YR	YR	YR	YR	h	semaphor	in IV
GRRL	FLQV	GANN	YR	YR	YR	YR	YR	h	semaphor	in V
NNRPI	V	IKTD	VN	YQ	FTQ	FTQ	FTQ	h	semaphor	in II

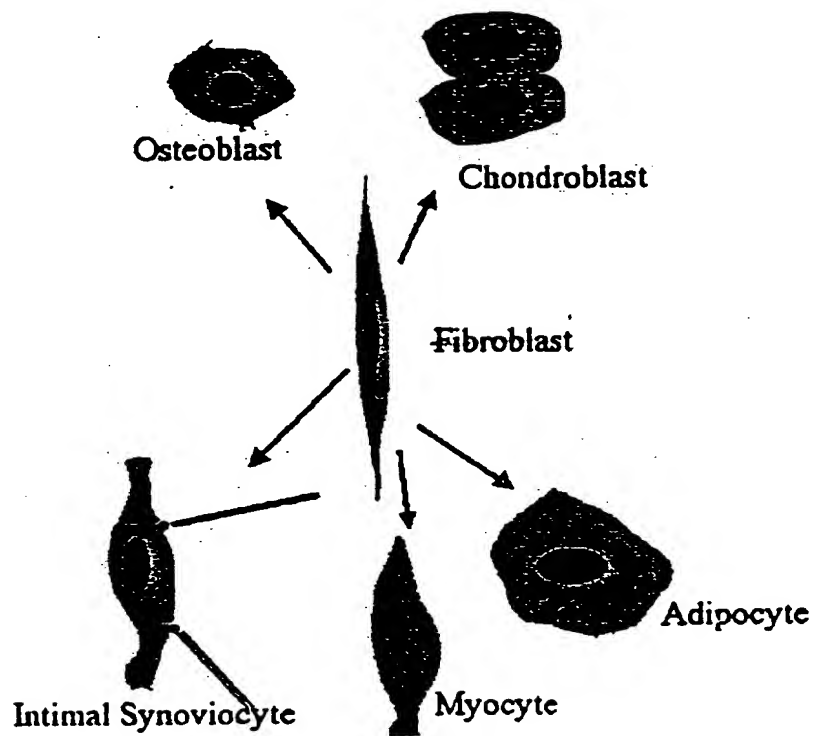
FIG. 4

RA OA RA OA RA OA RA OA RA OA RA OA RA OA



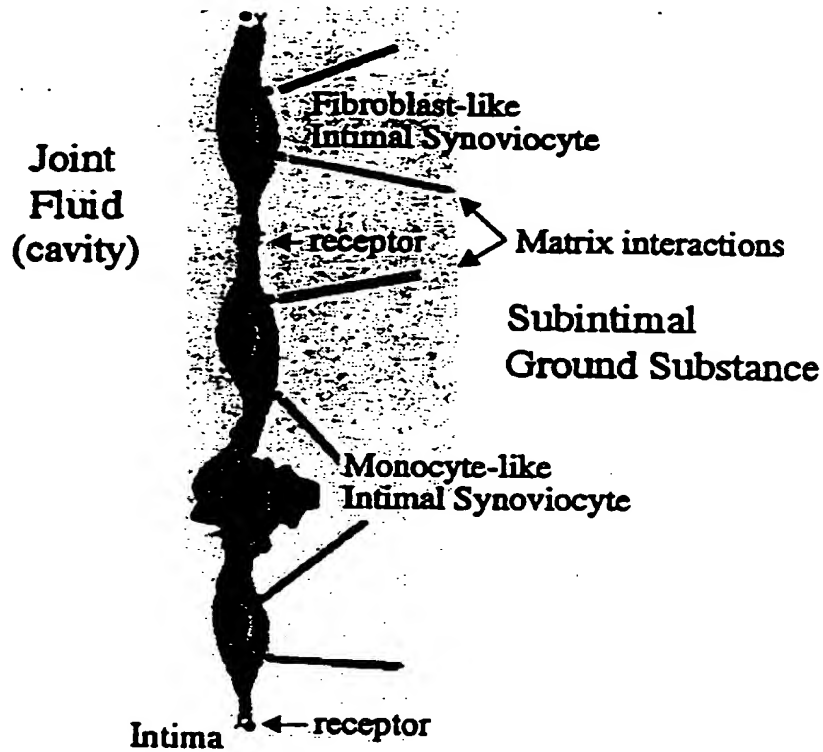
ML2122 ML2115 lumican IGFBP5 SDF1a semVI collagenaseIV

FIGURE 5



09500745 1020900

FIGURE 6



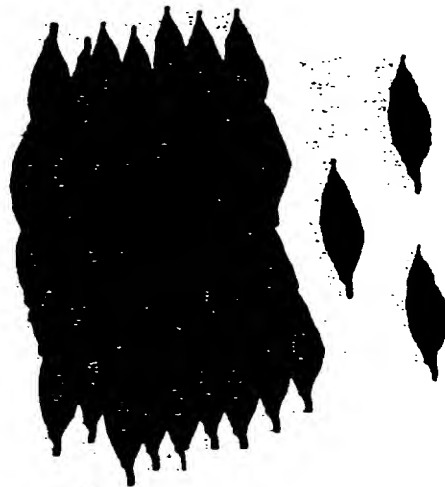
006020" 94200560

FIGURE 7



0

FIGURE 8



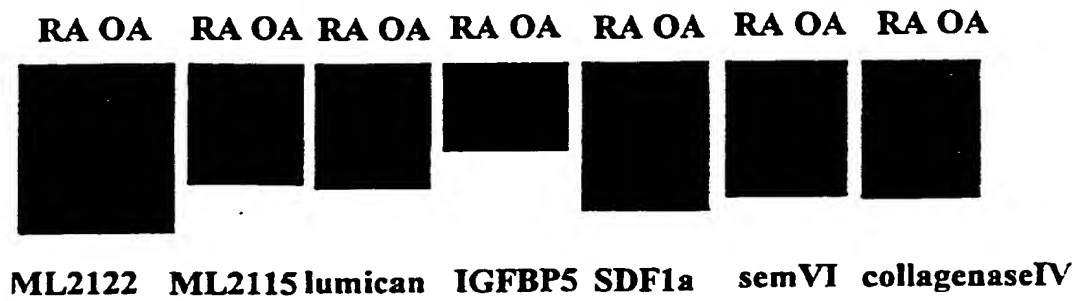
Fibroblast-like intimal
synoviocytes hyperplasia



Subintimal fibroblast-like
synoviocyte predominance

09500745 020900

FIGURE 9



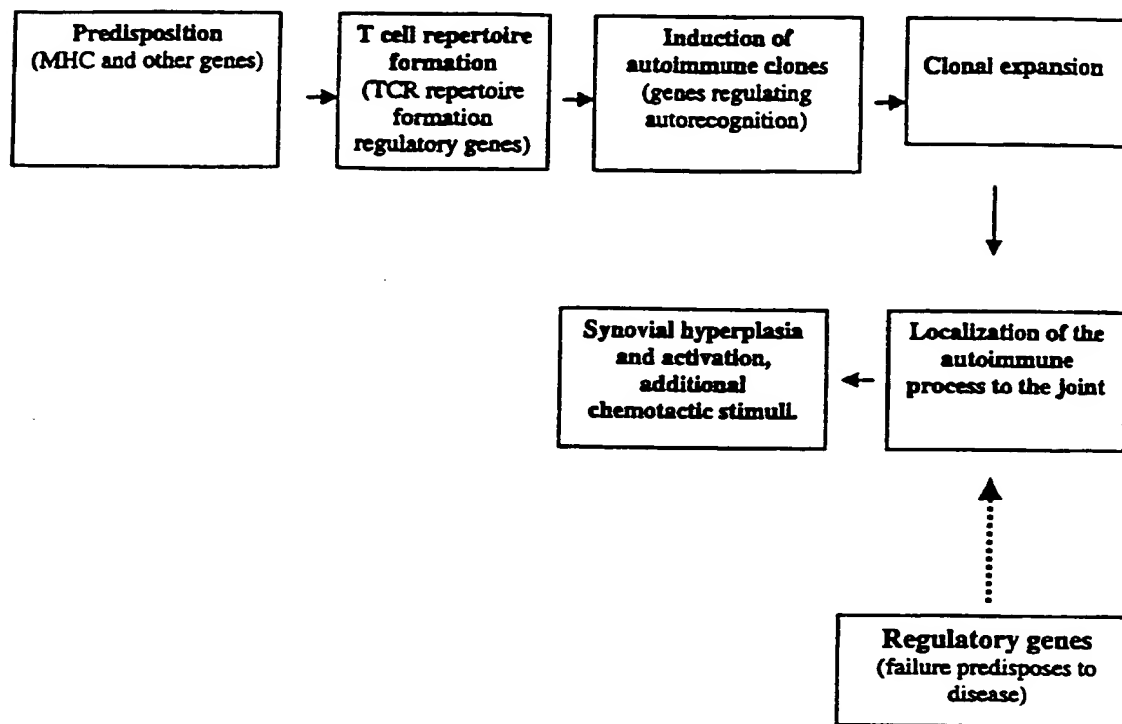
006020" 94200560

FIGURE 10

ROLLING selectins CD44	TRIGGERING chemokine-R integrins	TIGHT BINDING chemokine-R VCAM-1/ICAM-1 integrins	TRANSMIGRATION chemokine-R integrins
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006020 " 94/00560

FIGURE 11



006020" 9420960

FIGURE 12

10 20 30 40 50 60

New 95-04-12- 25.Seq(1>484) <- GNNAGAGTGTGGGACGGGGGNGNAGNAATTAAGGTAGNG-ATGGAGNANGGGGTGCNTNG
 New 95-04-12- 27.Seq(1>437) -> CCCGGGTACCGAGCTCGAATTCCGTTG
 GXXGAGTGTGGGACGGGGGXXGAXAATTAAGSYMGGGTAYSAGCWCGRRTSCGTTG

70 80 90 100 110 120

New 95-04-12- 25.Seq(1>484) <- GNNNAGANANTGNNTGGAGAANGACAANGGGGGGNGTCNNNGGAGGNGNTGTGA-GTGGG
 New 95-04-12- 27.Seq(1>437) -> NTGTCGCCGTTGN-TGTCG-----CAGATGCCCATGCCGATTCTTCGAAAGCCATGTTGC
 New 95-04-12- 01.Seq(1>382) -> CAGATGCCCATGCCGATTCTTCGAAAGCCATGTTGC
 New 95-03-30- 34.Seq(1>439) -> CAGATGNCCATGCCGATTCTTCGAAAGCCATGTTGC
 New 95-04-12- 21.Seq(1>466) <- CCATGTTCC
 GTGTMGMCRTTGXX-TGKMGaaxgaCAGATGSCCATGCCGATTCTTCGAAAGCCATGTTGC

130 140 150 160 170 180

New 95-04-12- 25.Seq(1>484) <- AAGAAGGCNACGTCAANAAGGACGAATATTTGCAANGNNGNNCAGGGCTGTNCNCGGGCA
 New 95-04-12- 27.Seq(1>437) -> CAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-AAA--CTGTGCCCTT-CA
 New 95-04-12- 01.Seq(1>382) -> CAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-AAA--CTGTGCCCTT-CA
 New 95-03-30- 34.Seq(1>439) -> CAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-AAA--CTGTGCCCTT-CA
 New 95-04-12- 21.Seq(1>466) <- AAGA-NCCA-CGTCAA-CATCCAAA-AT-CTCAACACNCC-CAA--CTNTTCCCTT-CA
 MAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-MAA--CTGTGCCCTT-CA

190 200 210 220 230 240

New 95-04-12- 25.Seq(1>484) <- GTTTGTAAAAAANAAGAACNGCGACAGACAAGTGTNNG-TTGACCCGAAGC-NA
 New 95-04-12- 27.Seq(1>437) -> GATTGTAGCCCGCTGAAGAACAACAAC-A--GACAAGTGTGCA-TTGACCCGAAGCTAA
 New 95-04-12- 01.Seq(1>382) -> GATTGTAGCCCGCTGAAGAACAACAAC-A--GACAAGTGTGCA-TTGACCCGAAGCT-A
 New 95-03-30- 34.Seq(1>439) -> GATTGTAGCCCGCTGAAGAACAACAAC-A--GACAAGTGTGCA-TTGACCCGAAGCT-A
 New 95-04-12- 21.Seq(1>466) <- GATTGTAGCCCGCTGAAGAACAACAAC-A-AGACAAGTGTGCATTTGACCCGAAGCTAA
 GATTGTAGCCCGCTGAAGAACAACAAC-A-aGACAAGTGTGCA-TTGACCCGAAGCTaa

250 260 270 280 290 300

New 95-04-12- 25.Seq(1>484) <- NAGTGGATNCAGGAGTACC-TGGAGNNA-CTATGAACAANTAAGCGCAACAGCC-AAAG
 New 95-04-12- 27.Seq(1>437) -> A-GTGGATTTCAGGAGTACC-TGGAG-AAAGCTTTAAACAAGTAAGCACAACAGC-AAAA
 New 95-04-12- 01.Seq(1>382) -> AAGTGGATTTCAGGAGTACC-TGGAGTAAAGCTTTAAACAAGTAAGCACAACAG-CCAAAA
 New 95-03-30- 34.Seq(1>439) -> AAGTGGATTTCAGGAGTACC-TGGAGTAAAGCTTTAAACAAGTAAGCACAACAG-NCAAAA
 New 95-04-12- 21.Seq(1>466) <- AAGTGGATTTCAGGAGTACC-TGGAG-AAAGCTTTAAACAAGTAAGCACAACAGCCCAAAA
 AAGTGGATTTCAGGAGTACC-TGGAGkAAAGCTTTAAACAAGTAAGCACAACAGCcCAAAA

310 320 330 340 350 360

New 95-04-12- 25.Seq(1>484) <- AGGACTTTCGCTAGACCCACTCGAGGAAAACATAAACCTTGTGAGAGATGAAAGGNCAA
 New 95-04-12- 27.Seq(1>437) -> AGGACTTTCGCTAGACCCANTCGANGAAAACATAAACCTTGTGAGAGATGAAAGGGCAA
 New 95-04-12- 01.Seq(1>382) -> AGGACTTTCGCTAGACCCACTCGAGGAAAACATAAACCTTGTGAGAGATGAAAGGGCAA
 New 95-03-30- 34.Seq(1>439) -> AGGACTTTCGCTAGACCCACTCGAGGAAAACATAAACCTTGTGAGAGATGAAAGGGCAN
 New 95-04-12- 21.Seq(1>466) <- AGGACTTTCGCTAGACCCACTCGAGGAAAACATAAACCTTGTGAGAGATGAAAGGNCAA
 New 95-04-12- 19.Seq(1>463) <- AN-TGAAGGGCCAA
 AGGACTTTCGCTAGACCCACTCGAGGAAAACATAAACCTTGTGAGAGATGAAAGGSCAA

370 380 390 400 410 420

New 95-04-12- 25.Seq(1>484) <- AGACGTGGGGG-AGGGGGCCNTAAC-CA-TGAGGACCAGGTGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 27.Seq(1>437) -> AGACGTGGGGGGAGGGGGGCTTAAC-CA-TGAGGACCAGGTGTGTGTGT-NGGGTGGGGC
 New 95-04-12- 01.Seq(1>382) -> NGACGTGNGG-AGGGGGGCTTAACC-AT-GAGGACCAGGTGTGTGTGTGTGGGG-TGGG-I
 New 95-03-30- 34.Seq(1>439) -> TGTNTTGTGG-AGGGGGCCTTAACC-AT-GAGGACCAGGTGTGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 21.Seq(1>466) <- AGACGTGGGGG-AGGGGGCCTTAAC-CA-TGAGGACCAGGTGTGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 19.Seq(1>463) <- AGACGTGGGGG-AGGGGGCCTTAACCCATTGAGGACCAGNTGTGTGTGTGTGGGGTGGG-C
 WGACGTGKGG-AGGGGGSCCTTAACccAttGAGGACCAGGTGTGTGTGTGTGGGGTGGG-C

430 440 450 460 470 480

New 95-04-12- 25.Seq(1>484) <- ACATTG-ATCT-GGG-ATCGGGCCTGAGGTTTGCCAGCATTTAGACCCTGCATTTATAGC
 New 95-04-12- 27.Seq(1>437) -> ACATTGGATCTTN-G-ATCGGGCCTGAGGTTTGGCAGCATTTAGACCCTGGATTTAT-GN
 New 95-04-12- 01.Seq(1>382) -> ACATTGNATCTTGGG-ATCGGGCCTGAGGTTTNGGCAGAATTTNGNCCCTGNATTTATNGN
 New 95-03-30- 34.Seq(1>439) -> ACATNGNATCT-GGGTATCGGGCCTGAGGTTTGNACAGCATTTAGNCCCTGNATTTATNGC
 ACATTGxATCTtGGG-ATCGGGCCTGAGGTTTGSAGCATTTAGACCCTGSATTTATRG

430 440 450 460 470 480

New 95-04-12- 21.Seq (1>466) <- ACATTG-ATCT-GGG-ATCGGGCTGAGGTTTGCCAGCATTTAGACCCGTCATTTATAGC
New 95-04-12- 19.Seq (1>463) <- ACATTG-ATCT-GGG-ATCGGGCTGAGGTTTGCCAGCATTTAGACCCGTCATTTATAGC
ACATTGxATCTtGGG-ATCGGGCTGAGGTTTGSCAGCATTTAGACCCGTSATTTATRGC
490 500 510 520 530 540

New 95-04-12- 25.Seq (1>484) <- ATACGGTATGATATTGCAG
New 95-04-12- 27.Seq (1>437) -> ATACGNNIGATNINN
New 95-04-12- 01.Seq (1>382) -> ATCC
New 95-03-30- 34.Seq (1>439) -> ATACGGCATGATATTGCAGNTTAT-TTCATCCATGCCNCGTACCTGTGNACGTTGGGAC
New 95-04-12- 21.Seq (1>466) <- ATACGGTATGATATTGCAGCTTATATTTCATCCATGCC- TGACCTGTGCACGTTGGAAC
New 95-04-12- 19.Seq (1>463) <- ATACGGTATGATATTGCAGCTTATATTTCATCCATGCC- TGACCTGTGCACGTTGGAAC
ATACGGYATGATATTGCAGCTTATATTTCATCCATGCCxYGTACCTGTGCACGTTGGRAC
550 560 570 580 590 600

New 95-03-30- 34.Seq (1>439) -> TAG
New 95-04-12- 21.Seq (1>466) <- TTTTATTACTGGGGTTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTTCA-GACA
New 95-04-12- 19.Seq (1>463) <- TTTTATTACTGGGGTTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTTCAAG-CAG
TWKTATTACTGGGGTTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTTCAaGaCAG
610 620 630 640 650 660

New 95-04-12- 19.Seq (1>463) <- TTAGTTCCTTCATGATCATCACAATCATCATCATTCATTCTCATTTTCTCAATTTTAAATC-AAC
New 95-04-12- 17.Seq (1>461) <- GGTTCATCNCAATCATCATCATTCATTCTCATTTTCTCAATTTTAAATCCAAC
TTAGTTCCTTCATGRTCATCACAATCATCATCATTCATTCTCATTTTCTCAATTTTAAATCCaAAC
670 680 690 700 710 720

New 95-04-12- 19.Seq (1>463) <- GAGTACTTCAAGATCTGAATTTGGCTTGTTTGGAGCATCTCCTCTGCTCCCCCTGGGGAGT
New 95-04-12- 17.Seq (1>461) <- GAGTACNTCAAGATCTG-ATTTGGCTTGTTTGGAGCATCTCCTCTGCTCCCCCTGGGGAGT
GAGTACTTCAAGATCTGaATTTGGCTTGTTTGGAGCATCTCCTCTGCTCCCCCTGGGGAGT
730 740 750 760 770 780

New 95-04-12- 19.Seq (1>463) <- CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGCCTTTCTTCAGACA
New 95-04-12- 17.Seq (1>461) <- CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGCCTTTCTTCAGACA
New 95-03-30- 09.Seq (1>445) -> GGGAGCTGGAAAAAGTGCCTTTCTTCAGACA
CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGCCTTTCTTCAGACA
790 800 810 820 830 840

New 95-04-12- 19.Seq (1>463) <- CTGAGGCTCCCGCAGCAGCGCCCTCCCAAGAGGAAGG
New 95-04-12- 17.Seq (1>461) <- CTGAGNCTCCCGCAGCAGCGCCCTCCCAAGAGGAAGGCCCTCTGTGGCACTCAGATACCG
New 95-03-30- 09.Seq (1>445) -> CTGAGGCTCCCGCAGCAGCGCCCTCCCAAGAGGAAGGCCCTCTGTGGCACTCAGATACCG
CTGAGGCTCCCGCAGCAGCGCCCTCCCAAGAGGAAGGCCCTCTGTGGCACTCAGATACCG
850 860 870 880 890 900

New 95-04-12- 17.Seq (1>461) <- ACTGGGGCTGGGCGCCGCCACTGCCTTCACCTCCTCTTTCAACCTCAGTGATTGGCTCTG
New 95-03-30- 09.Seq (1>445) -> ACTGGGGNTGGGCGCCGCCACTGNCTTCACCTCCTCTTTCAACCTCAGTGATTGGCTCTG
ACTGGGGCTGGGCGCCGCCACTGCCTTCACCTCCTCTTTCAACCTCAGTGATTGGCTCTG
910 920 930 940 950 960

New 95-04-12- 17.Seq (1>461) <- TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCCAGCTA
New 95-03-30- 09.Seq (1>445) -> TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCCAGCTA
New 95-04-12- 03.Seq (1>447) -> CCCAGCTA
TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCCAGCTA
970 980 990 1000 1010 1020

New 95-04-12- 17.Seq (1>461) <- TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG
New 95-03-30- 09.Seq (1>445) -> TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG
New 95-04-12- 03.Seq (1>447) -> TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG
TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG

			1030	1040	1050	1060	1070	1080
New 95-04-12- 17. Seq (1>461)	<-	TAGCCTGATCAGCGCCGACCAGCCGGAAGAGGGTGATTGCTGGGGCTCGTGCC						
New 95-03-30- 09. Seq (1>445)	->	TAGNCTGATCAGNGCCGACCAGCCGGAAGAGGGTGATTGCTGGGGCTCGTGCCCTGCA						
New 95-04-12- 03. Seq (1>447)	->	TAGCCTGATCAGCGCCGACCAGCCGGAAGAGGGTGATTGCTGGGGCTCGTGCCCTGCA						
New 95-04-12- 11. Seq (1>463)	<-						AG-TCGTGCCCTGCA	
New 95-04-12- 07. Seq (1>453)	->						TGCCCTGCA	
		TAGCCTGATCAGCGCCGACCAGCCGGAAGAGGGTGATTGCTGGGGCTCGTGCCCTGCA						
			1090	1100	1110	1120	1130	1140
New 95-03-30- 09. Seq (1>445)	->	TCCCTCTCC-TCCCAGGGGCTGNCCCAC-AGNTC-GGGCCCT-CTGTGAGATCCG--CTT						
New 95-04-12- 03. Seq (1>447)	->	TCCCTCTCC-TCCCAGGGGCTGCCCCAC-AGCTC-GGGCCCT-CTGTGAGATCCGT-CTT						
New 95-04-12- 11. Seq (1>463)	<-	TCCCTCTCCCTCCCAGGNCCTTCCCCACAAGCTCGGGGCCCT-CTGTGAGACCCGT-CTT						
New 95-04-12- 07. Seq (1>453)	->	TCCCTCTCC-TCCCAGGGGCTGCCCCAC-AGCTC-GGGCCCT-CTGTGAGATCCGT-CTT						
New 95-04-12- 05. Seq (1>475)	->						CGACGNCAGTGCCAAGCTTGCAI	
		TCCCTCTCC-TCCCAGGGGCTGCCCCAC-AGCTC-GGGCCCT-CTGTGAGAHCCGT-CTT						
			1150	1160	1170	1180	1190	1200
New 95-03-30- 09. Seq (1>445)	->	TNGG-CTCCTCCAGAATGG-GNTGGCCC-CTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
New 95-04-12- 03. Seq (1>447)	->	T-GGCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
New 95-04-12- 11. Seq (1>463)	<-	T-GCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCCTGCT						
New 95-04-12- 07. Seq (1>453)	->	T-GGCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
New 95-04-12- 05. Seq (1>475)	->	---GCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
		T-GGCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
			1210	1220	1230	1240	1250	1260
New 95-03-30- 09. Seq (1>445)	->	TAG						
New 95-04-12- 03. Seq (1>447)	->	TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
New 95-04-12- 11. Seq (1>463)	<-	TACCCCAAAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
New 95-04-12- 07. Seq (1>453)	->	TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
New 95-04-12- 05. Seq (1>475)	->	TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
		TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
			1270	1280	1290	1300	1310	1320
New 95-04-12- 03. Seq (1>447)	->	TTGAGTGACTGGGTTTTGGTGATTGNCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
New 95-04-12- 11. Seq (1>463)	<-	TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
New 95-04-12- 07. Seq (1>453)	->	TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
New 95-04-12- 05. Seq (1>475)	->	TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
		TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
			1330	1340	1350	1360	1370	1380
New 95-04-12- 03. Seq (1>447)	->	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAA-TCAGTGAATAAACCATCATCTTGCC						
New 95-04-12- 11. Seq (1>463)	<-	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGCC						
New 95-04-12- 07. Seq (1>453)	->	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGNC						
New 95-04-12- 05. Seq (1>475)	->	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGCC						
		AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGSC						
			1390	1400	1410	1420	1430	1440
New 95-04-12- 03. Seq (1>447)	->	ACTA-CCCCTCCTGAAGC-ACAGNAGGGTT						
New 95-04-12- 11. Seq (1>463)	<-	ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCAATC-AGAAGTGTGGC-AAG						
New 95-04-12- 07. Seq (1>453)	->	ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCAATC-AGAAGTGTGG-CAAG						
New 95-04-12- 05. Seq (1>475)	->	ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCAATC-AGAAGTGTGG-CAAG						
New 95-03-30- 03. Seq (1>376)	<-						CNA-NNAGAACTGTTGCCCG-G	
New 95-03-30- 30. Seq (1>377)	<-						GATCAAGGGCTGTTGGCCGAG	
New 95-04-12- 09. Seq (1>381)	->						CTGTTGGCA-AG	
		ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCRATCaAGAAGTGTGGcCRAG						
			1450	1460	1470	1480	1490	1500
New 95-04-12- 11. Seq (1>463)	<-	GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCCTGGT-GGTATTT-GTAACCTI						
New 95-04-12- 07. Seq (1>453)	->	GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCCTGGTGGGTATTTGGTAACCTI						
New 95-04-12- 05. Seq (1>475)	->	GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCCTGGTGGGTATTTGGTAACCTI						
		GT-GACATTTCCATGCATAAATGCGAWCCACAGRRGGKCCTGGKgGGTATTTgGTAACYI						

1450 1460 1470 1480 1490 1500

New 95-03-30- 03.Seq(1>376) <- GT-GACATTTCCATNCATAAATGCGAACCACAGNNGGNCC-NGGNGGNA-TT-TNTACCT
New 95-03-30- 30.Seq(1>377) <- GTGGNAATTTCCATNCANAAATGCGAACCCAGGGGGGCGGGGGGNA-TT-GTAACCT
New 95-04-12- 09.Seq(1>381) -> GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCTGGT-GGTATTT-GTAACTT
GT-GACATTTCCATGCATAAATGCGAWCCACAGRRGGKCCCTGGKgGGTATTTgGTAACYT

1510 1520 1530 1540 1550 1560

New 95-04-12- 11.Seq(1>463) <- TTTGCAAGGCATTTTTTTTATATATAT-TTTTGTGGGCA
New 95-04-12- 07.Seq(1>453) -> TTNGGAAGGNATTTNNNNATATATAT-TTTNGGGAN
New 95-04-12- 05.Seq(1>475) -> TTGGNAAGGC-A-TTTNNNNATATATATTTNGGGGCACATTTTTTTTTTACGTTTCTTTT
New 95-03-30- 03.Seq(1>376) <- TTTNCCAGGCAN-TTTTTTAAAAAAAANTTTGT-NCANATTTTTTTTNTACGNITCNTNA
New 95-03-30- 30.Seq(1>377) <- TTTTCCAGGNAATTTTTTAAAAAAA-NTTTGT-GCACANTTTTTTTTTNCGNITCNTNA
New 95-04-12- 09.Seq(1>381) -> TTTGNAAGGCATTTTTTTATATATAT-TTTTGNG-CACATTTTTTTTTTACGTTTCTTTA
TTKSMAGGCATTTTTTAWAWAWAWaTTTTGKgrSAMATTTTTTTTTTACGTTTCTTTA

1570 1580 1590 1600 1610 1620

New 95-04-12- 05.Seq(1>475) -> AGAAACAAATGT-TTTCAAAATNT-TTTAT-GGTCGACAATCAAT
New 95-03-30- 03.Seq(1>376) <- GNAANCCAATGTATTCCCCAANATATTTANANGCGGACAANTC--ANATANTTGGAGTGG
New 95-03-30- 30.Seq(1>377) <- GGANGCCNATNNATNCCCCCANATGTTTATAGGCGNANAAAAA--AAAAATTTGGGGNGG
New 95-04-12- 09.Seq(1>381) -> GAAACAAATGTATTTCAAAATATATTTATAGTCGAACAAATTCAT--ATATTTGAAGTGG
GRAARCMAATGTATTTCMMAATATRTTTATAGGCGRACAAWHMatAaAWATTTGRRGTGG

1630 1640 1650 1660 1670 1680

New 95-03-30- 03.Seq(1>376) <- ANCCAAATGGATNTCAGTAGTTTAAACNTCTCTANTATCCCCAACNGCTGGCCANTTTNTT
New 95-03-30- 30.Seq(1>377) <- NGCCAANTGGATTTTCAGGAGNTNAAACCTCNCNANTATCCCCNCCNCTGGCCATTTTTTT
New 95-04-12- 09.Seq(1>381) -> AGCCATATGAATGTCAGTAGTTTATACTTCTCTATTATCTCAAACACTGGAATTTGTA
AGCCAWATGRATKTCAGKAGTTTAWACYTCTCTAXTATCYCMAACYRCTGGCMATTTKTW

1690 1700 1710 1720 1730 1740

New 95-03-30- 03.Seq(1>376) <- NAGNAANAAANATGAAAAANGAATNTGGTTTCAGCNTTTCCATNTTAACNCAGTNGATT
New 95-03-30- 30.Seq(1>377) <- AAGGNAAAAAAATGAAAAANNGAATNTGGTTTCAGCCTTTCCATNTTAACNCAGTNNAAI
New 95-04-12- 09.Seq(1>381) -> AAGAAATATATATGATATATAAATGTGATTGCAGCTTTTCAATGTTAGCCACAGTGTATT
AAGRAAWAWAWATGAWAWAXRRATXTGRTTKCAGCYTTTCMATXTTARCCXCAGTXKAWI

1750 1760 1770 1780 1790 1800

New 95-03-30- 03.Seq(1>376) <- TTTTCACTTNTNCCAAAATNTTACCCNATNTNACANTAAATNCCCTANCNAANAATTCN
New 95-03-30- 30.Seq(1>377) <- TTTTCNCTTNNNCCNNAATTTNNCCCCATNTNGCNTTAAATTTCCCNANCCAAANAATNCN
New 95-04-12- 09.Seq(1>381) -> TTTTCACTTGTACTAAAATTTGTATCAAATGTGACATTATATGCACTAGCAATAAAATGCT
TTTTCACTTXXTCYAAAATTTXTAYCMMATXTXRCATTAWATKCMCTAXCMAWAAAATKXC

1810

New 95-03-30- 03.Seq(1>376) <- GATT
New 95-03-30- 30.Seq(1>377) <- NA
New 95-04-12- 09.Seq(1>381) -> AATTGTTTCATGGGTAA
RATGTTTCATGGGTAA